

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/779,599DATE: 03/04/97  
TIME: 13:58:01

INPUT SET: S15900.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Goeddel, David V.  
6 Rothe. Mike  
7  
8 (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors  
9  
10 (iii) NUMBER OF SEQUENCES: 59  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Genentech, Inc.  
14 (B) STREET: 460 Point San Bruno Blvd  
15 (C) CITY: South San Francisco  
16 (D) STATE: California  
17 (E) COUNTRY: USA  
18 (F) ZIP: 94080  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: WinPatin (Genentech)  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER:  
28 (B) FILING DATE: 07-Jan-1997  
29 (C) CLASSIFICATION:  
30  
31 (viii) ATTORNEY/AGENT INFORMATION:  
32 (A) NAME: Dreger, Ginger R.  
33 (B) REGISTRATION NUMBER: 33,055  
34 (C) REFERENCE/DOCKET NUMBER: P0897C2  
35  
36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: 415/225-3216  
38 (B) TELEFAX: 415/952-9881  
39 (C) TELEX: 910/371-7168  
40  
41 (2) INFORMATION FOR SEQ ID NO:1:  
42  
43 (i) SEQUENCE CHARACTERISTICS:  
44 (A) LENGTH: 2088 base pairs  
45 (B) TYPE: Nucleic Acid  
46 (C) STRANDEDNESS: Single

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47 (D) TOPOLOGY: Linear

48

49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50

51

52 CCCAGCCCCG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50

53

54 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100

55

56 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150

57

58 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200

59

60 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250

61

62 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300

63

64 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350

65

66 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400

67

68 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450

69

70 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTGGCTGT TCCTTCAAGG 500

71

72 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550

73

74 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600

75

76 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650

77

78 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700

79

80 CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750

81

82 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

83

84 ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850

85

86 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900

87

88 GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950

89

90 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000

91

92 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050

93

94 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100

95

96 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150

97

98 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200

99

RAW SEQUENCE LISTING  
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100 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250  
101  
102 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300  
103  
104 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350  
105  
106 CGGCTGCCCC CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400  
107  
108 CCTACGTCAA AGATGACACA ATGTTCTCTCA AATGCATTGT GGACACTAGT 1450  
109  
110 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500  
111  
112 GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550  
113  
114 CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600  
115  
116 GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650  
117  
118 GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700  
119  
120 GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750  
121  
122 GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800  
123  
124 AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850  
125  
126 TGGAAAAATG CCCCCATCTC TCTGTTTCTG CTCAAACTA GAACCACAGG 1900  
127  
128 GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950  
129  
130 CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAACTG CCCTGGGAAA 2000  
131  
132 TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTACC GACAAAACAA 2050  
133  
134 ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAAA 2088  
135

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

145 Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly  
146 1 5 10 15  
147  
148 Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu  
149 20 25 30  
150  
151 Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp  
152 35 40 45

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153	
154	Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser
155	50 55 60
156	
157	Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala
158	65 70 75
159	
160	Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe
161	80 85 90
162	
163	Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln
164	95 100 105
165	
166	Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys
167	110 115 120
168	
169	Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu
170	125 130 135
171	
172	Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr
173	140 145 150
174	
175	Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser
176	155 160 165
177	
178	Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu
179	170 175 180
180	
181	Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala
182	185 190 195
183	
184	Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala
185	200 205 210
186	
187	Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu
188	215 220 225
189	
190	Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp
191	230 235 240
192	
193	Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu
194	245 250 255
195	
196	Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr
197	260 265 270
198	
199	Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe
200	275 280 285
201	
202	Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu
203	290 295 300
204	
205	Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu

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206		305		310		315
207						
208	Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu					
209		320		325		330
210						
211	Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln					
212		335		340		345
213						
214	Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser					
215		350		355		360
216						
217	Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser					
218		365		370		375
219						
220	Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys					
221		380		385		390
222						
223	His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val					
224		395		400		405
225						
226	Asp Thr Ser Ala					
227		409				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2121 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

237	
238	
239	
240	GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50
241	
242	GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100
243	
244	CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150
245	
246	CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200
247	
248	CGCTACTGCT CTTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250
249	
250	CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300
251	
252	TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCCGAG AGAGGTGGAG 350
253	
254	AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400
255	
256	GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTG CTGCTGACGG 450
257	
258	AGTGTCTGCT ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500

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**SEQUENCE VERIFICATION REPORT**  
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Error

Original Text